Amendment to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1. (currently amended) A computer-implemented method of determining a statistical model for predicting disease risk for a member of a population, comprising:

    collecting, at least one computing device, a plurality of sets of data, each of said sets of data associated with one member of said population, and comprising non-genetic data of a first type, genetic data of a second type, and an indicator of disease status of said one member associated with said set;

    storing at least one computing device selecting a candidate statistical model for calculating said disease risk as a function of non-genetic data of said first type, said candidate model dependent on a plurality of parameters;

    determining, by at least one computing device, a plurality of weights, each one of said weights associated with one of said sets of data and indicating a statistical significance of said one of said sets of data, wherein weights associated with sets of said data having like genetic data of said second type are the same; and

    optimizing, by at least one computing device, said parameters of said candidate model by fitting said plurality of sets of data to said candidate model, wherein said fitting comprises:

    calculating for each of said sets, a deviate of a predicted risk from an indicator of disease status for that set, said predicted risk predicted using said candidate model and non-genetic data in that set;

    calculating a sum of weighted deviates for all of said sets, wherein each deviate is weighted in said sum by the weight associated with that set for which said each deviate has been calculated; and

    minimizing said sum of weighted deviates to obtain optimized parameters,

    taking into account said weights, and choosing said candidate statistical model with said parameters so optimized as a risk model so that a risk calculated using

said ~~risk~~ candidate model with said optimized parameters and non-genetic ~~a set of~~ data ~~of said first type~~ associated with a particular member of said population is indicative of a disease risk to said particular member.

2. (currently amended) The method of claim 1, wherein said deviate is a difference between said predicted risk and said indicator of disease status~~data of said first type is non-genetic data and data of said second type is genetic data~~.

3. (currently amended) The method of claim 1, wherein each weighted deviate is a product of the corresponding weight and a function of the corresponding deviate~~said weights are used to assess a goodness of said fitting~~.

4. (currently amended) The method of claim 1, wherein said determining comprises:

    grouping said collected data into groups such that all sets of data within each said group have like genetic data ~~of said second type~~, one of said groups being a reference group which contains sets of data having genetic data ~~of said second type~~ like genetic data ~~of said second type~~ obtained from said member of said population; and

    determining a group weight for each said group, whereby said group weight is the corresponding weight for each set of data within said each group.

5. (original) The method of claim 4, wherein the group weight of said reference group has a value of one and each of the other group weights has a value between zero and one.

6. (original) The method of claim 5, wherein said other group weights are optimized by minimizing a target function, said target function dependent on a plurality of residuals, one of said residuals for each of the data sets in said reference group.

7. (previously presented) The method of claim 6, wherein a residual for an ith one of said data sets in said reference group is the difference between a value of the indicator of disease status contained in said ith data set and the value of disease risk for the member associated with said ith data set, said value of disease risk calculated from said candidate model with said parameters optimized for a given set of group weights by fitting data sets in groups other than the reference group to said candidate model.

8. (original) The method of claim 7, wherein said target function is of the form:

$$f = \sum w_i \phi(r_i),$$

where

w_i is the corresponding weight for data set i; and

r_i is the residual for data set i.

9. (currently amended) The method of claim 1, wherein said non-genetic data of said first type comprises data indicative of time.

10. (original) The method of claim 9, wherein said candidate model is a Cox proportional hazard regression model.

11. (original) The method of claim 9, wherein said candidate model is a disease risk function of the form:

$$R(t) = 1 - \exp\{-\int_0^t h(u)du\},$$

where

$R(t)$ represents said disease risk at a given time t;

$h(u)$ is of the form:

$$h(u) = h_0(u)\exp(\sum_1^{n_c} \beta_i x_i);$$

$h_0(u)$ is dependent only on u;

x_i is a variable indicative of a disease risk factor, said collected data containing a plurality of values of x_i;

β_i is a coefficient for x_i; and

n_c is the number of coefficients in said disease risk function.

12. (original) The method of claim 1, wherein said collecting comprises imputing missing data to said plurality of data sets.

13. (currently amended) The method of claim 1, wherein each one of said plurality of said weights is weighted by an adjustment factor indicative of ~~a representativeness of~~ <u>an extent to which</u> the member associated with said each one of said plurality of said weights <u>is representative of members of</u> [[in]] said population.

14. (original) The method of claim 13, wherein an adjustment factor a_i for a data set obtained from a member i of said population is calculated as:

$$a_i = \frac{n_i^p}{n_i^s},$$

where n_i^p is the number of members in said population who share a same set of characteristics with said member i, and n_i^s is the number of members associated with said collected data who share said set of characteristics.

15. (original) The method of claim 14, wherein said set of characteristics comprises non-genetic factors.

16. (withdrawn) The method of claim 14, wherein said set of characteristics comprises genetic factors.

17. (original) The method of claim 14, wherein said set of characteristics comprises both genetic and non-genetic factors.

18. (original) The method of claim 14, wherein said set of characteristics are selected from the group of age, gender, race, body mass index, smoking status, hypertension, cholesterol level, personal health history, and family health history.

19. (currently amended) The method of claim 1, comprising calculating ~~a disease~~ <u>said</u> risk for said <u>particular</u> member of said population <u>using said candidate model</u> with said <u>optimized parameters</u> ~~disease risk prediction model~~.

20. (currently amended) A computing system <u>comprising at least one computing device,</u> adapted for performing the method of any one of claims 1 to 19.

21. (currently amended) An article of manufacture comprising a computer readable medium embedded thereon computer executable instructions, which when executed by a computer causes said computer to determine a statistical model for predicting disease risk for a member of a population by

collecting a plurality of sets of data, each of said sets of data associated with one member of said population, and comprising non-genetic data of a first type, genetic data of a second type, and an indicator of disease status of said one member associated with said set;

storing selecting a candidate statistical model for calculating said disease risk as a function of non-genetic data of said first type, said candidate model dependent on a plurality of parameters;

determining a plurality of weights, each one of said weights associated with one of said sets of data and indicating a statistical significance of said one of said sets of data, wherein weights associated with sets of said data having like genetic data of said second type are the same;

optimizing said parameters of said candidate model by fitting said plurality of sets of data to said candidate model, wherein said fitting comprises:

calculating for each of said sets, a deviate of a predicted risk from an indicator of disease status for that set, said predicted risk predicted using said candidate model and non-genetic data in that set;

calculating a sum of weighted deviates for all of said sets, wherein each deviate is weighted in said sum by the weight associated with that set for which said each deviate has been calculated; and

minimizing said sum of weighted deviates to obtain optimized parameters,

taking into account said weights; and storing said candidate statistical model with said parameters so optimized as a risk model such so that a risk calculated using said risk candidate model with said optimized parameters and non-genetic a set of data of said first type associated with a particular member of said population is indicative of a disease risk to said particular member.

22. (previously presented) The method of claim 1, wherein each of said sets of data is indicative of a plurality of factors, and said collecting comprises:

determining a correlation between said plurality of factors;

grouping said factors into batches such that all factors in each said batch are correlated; and

imputing missing data for factors in one said batch at a time.

23. (currently amended) The method of claim 4, wherein said grouping comprises:

dividing said plurality of sets of data into two or more groups depending on data indicative of a <u>non-genetic</u> factor ~~of said first type~~ in each of said data sets;

determining if a criterion is met after said dividing, said criterion is evaluated based on <u>genetic</u> data ~~of said second type~~ in each of said data sets; and

when said criterion is not met, regrouping said plurality of sets of data back into one group.

24. (original) The method of claim 23, wherein said dividing is performed recursively on each group of a division.

25. (original) The method of claim 24, wherein divisions at different levels are made dependent on data indicative of different factors.

26. (original) The method of claim 25, wherein a branch of said recursive division is terminated at the level at which said criterion is not met.

27. (currently amended) A <u>computer-implemented</u> method of weighing a plurality of data sets, each one of said data sets associated with a member of a population, comprising:

weighing<u>, by at least one computing device,</u> each set of said plurality of data sets by a weight indicative of a representativeness of the member associated with said each set in said population, wherein a weight a_i for a data set obtained from a member i of said population is calculated as:

$$a_i = \frac{n_i^p}{n_i^s},$$

where n_i^p is the number of members in said population who share a same set of characteristics with said member i, and n_i^s is the number of members associated with said collected data who share said set of characteristics; and

storing, at least one computing device, said weight a_i in association with said data set obtained from said member i.

28. (new) A computer-implemented method of determining a statistical model for predicting disease risk for a member of a population,

storing, at least one computer, a plurality of statistical models, each for calculating said disease risk;

for each of said models, assessing, by at least one computer, a goodness of fit of data derived from a plurality of members of said population, said assessing comprising calculating

a deviate from an indicator of a disease status of each member by a predicted risk for that member, predicted using that model and non-genetic data associated with that member, and

a sum of weighted deviates, each deviate weighted by a weight reflecting genetic data associated with that member for whom that deviate is calculated; and

selecting the model that produces the lowest sum of weighted deviates as a risk prediction model for predicting said disease risk.

29. (new) The method of claim 28, wherein each of said models is dependent on a plurality of parameters, different ones of said models having different numbers of parameters.

30. (new) The method of claim 28, wherein each of said models is dependent on a plurality of parameters, different ones of said models having an equal number of parameters.